Proceeding
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An Assessment of Genetic Variation of *Pinus albicaulis* Populations from Oregon and Washington in Relation to Height Increment, Phenology, and Form

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Abstract – It is desirable to ascertain patterns of genetic variation associated with provenance origin for any species that warrants intensive conservation efforts. Whitebark pine (*P. albicaulis*) is a species in the western United States that is currently experiencing a major dcline in health (accelerated mortality from cumulative effects of disease, bark beetles, and additional environmental stresses). Very little common garden data is available on whitebark pine from any part of its range (Mahalovich *et al.* 2006) or from Oregon and Washington provenances (Bower and Aitken 2008).

A complementary study to a planned white pine blister rust resistance evaluation experiment at the Dorena Genetic Resource Center was undertaken in order to evaluate genetic variation of height growth increment in whitebark pine (*P. albicaulis*). The study included a total of 100 families from 6 provenances located in Oregon and Washington with a variable number of parent trees (families) per provenance (Table 1). Wind-pollinated seed was sown in a container nursery in 2004 and then transplanted to a common garden raised bed for future assessment of disease resistance. Seedlings were inoculated with blister rust in September 2005, and height and phenology assessments were made from April 2006 - July 2006 before any adverse effects of the rust were noted. The experimental design was a randomized complete block with families planted in row-plots (up to 10 trees/family/plot). Phenology patterns, relative growth rates, total growth increment, and tree stem form were assessed and quantified.

Table 1. Provenance locations and sample size (# parent trees) in the common garden study

Provenance	Latitude (°N)	Longitude (°W)	Elevation (m)	Sample Size (N)
1. Mt. Rainier	46.9	121.6	1859-1939	19
2. Mt. Hood	45.3	121.7	1832-1898	19
3. Warm Springs	44.7	121.7	1676	7
4. Crater Lake	42.9	122.1	2146-2164	9
5. Malheur	44.7	118.6	2233-2405	19
6. Umatilla	44.7	118.6	2289-2332	27

The common garden locale was located near Cottage Grove, Oregon: 43.7°N latitude, 122.9°W longitude, 128 m in elevation.

Eight serial height measurements were taken throughout the third growing season in three of the six replications. Cumulative height increment was computed as well as percent of total seasonal height growth and percent of growth cessation (where growth cessation was equated to $\geq$ 95% of total seasonal height growth) at each serial measurement. A score (1 = single stem, 2 = forked, or 3 = numerous multi-stems/bush) was also given for the general stem form of the seedlings at the end of the growing season. Statistical analysis procedures were conducted using SAS (SAS Institute v. 9.1, 2007); provenance was considered as a fixed effect, while block, family within provenance, and associated interactions were considered as random effects in the general linear model.

Least square means for all serial height increments differed significantly ($P < .05$) among provenances, and there was significant variation among families within provenances at all serial measurement times. The cumulative height increment rank changed among provenances until the third periodic measure, after which the provenances' general rankings remained the same throughout the rest of the growing season (Figure 1). The northwestern provenances (Mt. Hood, Mt. Rainier, Warm

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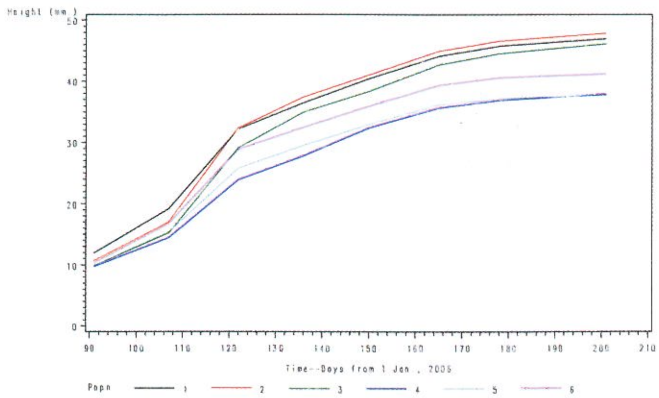

Figure 1. Cumulative height increment over time.

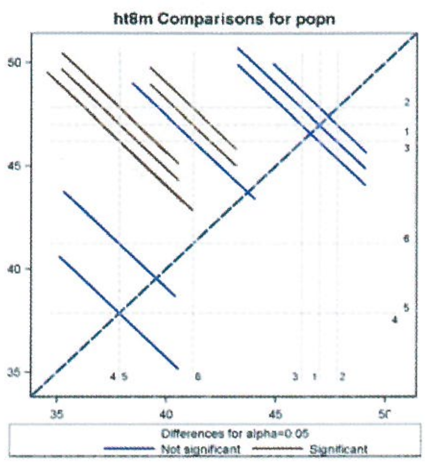

Figure 2. Statistical significance (P<.05) among provenance means for season's height increment. Height increment shown on vertical and horizontal axes (mm). Provenance (1...6) represent: Mt. Rainier=1, Mt. Hood=2, Warm Springs=3, Crater Lake=4, Malheur=5, Umatilla=6.

Springs) formed a general group with the maximum height. The Umatilla provenance was intermediate in height, followed by the Malheur and Crater Lake provenance grouping. Statistical comparisons among provenance means for total height increment is shown in the SAS - Proc Glimmix plot (Figure 2).

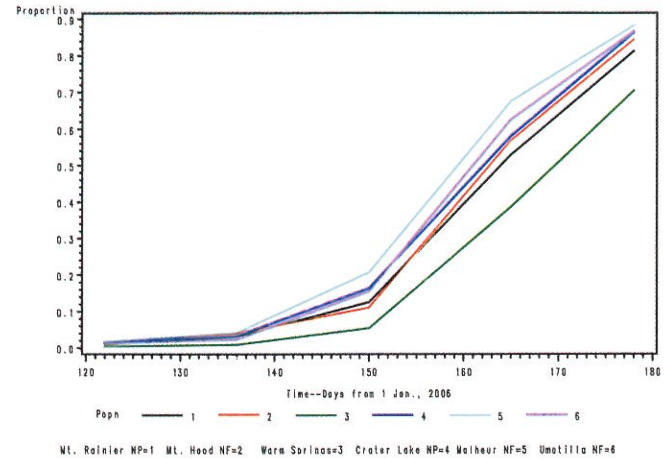

Figure 4. Proportion of growth cessation over time.

Individual tree heritability was 0.27 (family mean range = 25-64 mm for total height increment). The parent tree source environmental variables of elevation, longitude, latitude, and associated climatic means (average monthly high and low temperatures, precipitation) were assessed in a regression on total height increment. Precipitation (average amounts in September + February + November + May) explained 34% of the variation.

The percentage of the seasonal height growth completed (Figure 3a & b) and percentage of growth cessation (Figure 4) at each measurement date were also computed. Significant differences existed among provenances in the estimates of shoot elongation timing, where percent of growth completed at measurement times 1 and 2 was used as an indicator of initial growth (average family heritability=0.43 for the two measurement times). Twenty seven % of the variation was explained by temperature and latitude (average minimum temperature in December + (latitude)^2 + average maximum temperature in January) in a regression on the second serial measurement (mean range=35-42% of total seasonal growth).

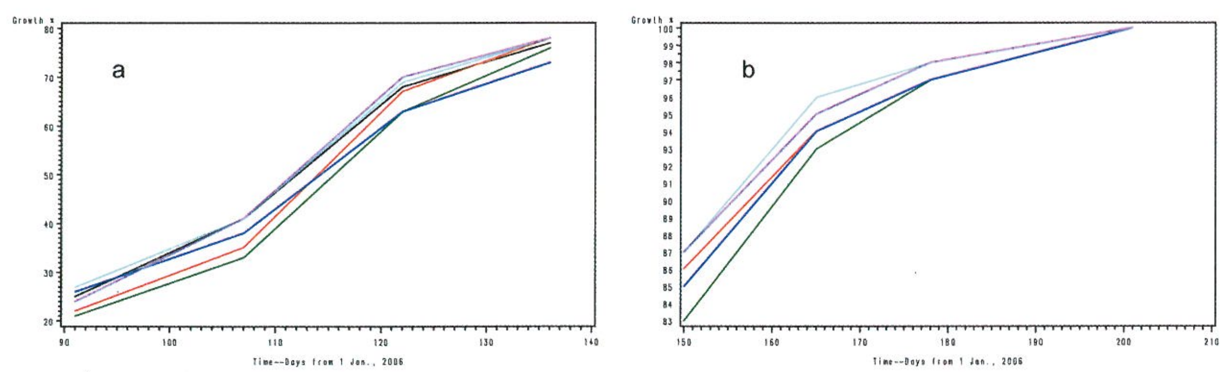

Figure 3. Percent of seasonal height increment completed over (a) early and (b) late season.

Significant differences existed among provenances in percentage of growth cessation at measurement times 5, 6, and 7 (average family heritability = 0.19). Twenty four % of the variation was explained by elevation + average maximum temperature in May for the sixth serial measurement (mean range = 39-67% cessation).

The least square means for stem form differed significantly among provenances. The rank order of the more desirable tree form class to the less desirable tree form class was closely aligned with the rank order (from tallest to shortest) of the final height per respective provenance.

Significant differences were noted among provenances in relation to height increment, relative percentage of growth completed and growth cessation during the season. These differences along with the low to moderate heritability estimates suggest a measurable degree of genetic adaptation across the sampled species range. These preliminary results indicate an adaptive response to the source elevation and latitude.

References

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